

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/812,393DATE: 04/28/98
TIME: 13:04:20

INPUT SET: S25310.raw

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: SHERMAN, Linda A.
6 LUSTGARTEN, Joseph
7
8 (ii) TITLE OF THE INVENTION: RECOMBINANT CONSTRUCTS ENCODING
9 T CELL RECEPTORS SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR
10 ANTIGENS
11
12 (iii) NUMBER OF SEQUENCES: 64
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: MORRISON & FOERSTER
16 (B) STREET: 2000 Pennsylvania Avenue, NW, suite 5500
17 (C) CITY: Washington
18 (D) STATE: DC
19 (E) COUNTRY: USA
20 (F) ZIP: 20006-1888
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Diskette
24 (B) COMPUTER: IBM Compatible
25 (C) OPERATING SYSTEM: DOS
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: 08/812,393
30 (B) FILING DATE: 05-MAR-1997
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER:
35 (B) FILING DATE:
36
37
38
39 (viii) ATTORNEY/AGENT INFORMATION:
40 (A) NAME: Murashige, Kate H
41 (B) REGISTRATION NUMBER: 29,959
42 (C) REFERENCE/DOCKET NUMBER: 31333-20001.00
43
44 (ix) TELECOMMUNICATION INFORMATION:
45 (A) TELEPHONE: 202-887-1500

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46 (B) TELEFAX: 202-822-0168
47 (C) TELEX:
48
49

ERRORED SEQUENCES FOLLOW:

250 (2) INFORMATION FOR SEQ ID NO:3:
251
252 (i) SEQUENCE CHARACTERISTICS:
253 (A) LENGTH: 24 base pairs
254 (B) TYPE: nucleic acid
255 (C) STRANDEDNESS: single
256 (D) TOPOLOGY: linear
257
258 (vi) ORIGINAL SOURCE:
--> 259 (C) ISOLATE: V-alpha-1) INDIVIDUAL ISOLATE :
260
261 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
262
263 CCCAAGGCAC TGATGTTCAT CTTC 24
264

globally replace -- repetitive error

265 (2) INFORMATION FOR SEQ ID NO:4:
266
267 (i) SEQUENCE CHARACTERISTICS:
268 (A) LENGTH: 27 base pairs
269 (B) TYPE: nucleic acid
270 (C) STRANDEDNESS: single
271 (D) TOPOLOGY: linear
272
273 (vi) ORIGINAL SOURCE:
--> 274 (C) ISOLATE: V-alpha-2
275
276 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
277
278 TGAGACAAAG TCCCCAATCT CTGACAG 27
279

280 (2) INFORMATION FOR SEQ ID NO:5:
281
282 (i) SEQUENCE CHARACTERISTICS:
283 (A) LENGTH: 26 base pairs
284 (B) TYPE: nucleic acid
285 (C) STRANDEDNESS: single
286 (D) TOPOLOGY: linear
287
288 (vi) ORIGINAL SOURCE:
--> 289 (C) ISOLATE: V-alpha-3
290

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291 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
292
293 CTGCAGCTGC TCCTCAAGTA CTATTC 26
294

295 (2) INFORMATION FOR SEQ ID NO:6:
296
297 (i) SEQUENCE CHARACTERISTICS:
298 (A) LENGTH: 28 base pairs
299 (B) TYPE: nucleic acid
300 (C) STRANDEDNESS: single
301 (D) TOPOLOGY: linear
302
303 (vi) ORIGINAL SOURCE:
--> 304 (C) ISOLATE: V-alpha-4.1.2.3
305
306 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
307
308 TCCCGGAGAA GGTCCACAGT TCCTCTTT 28
309

310 (2) INFORMATION FOR SEQ ID NO:7:
311
312 (i) SEQUENCE CHARACTERISTICS:
313 (A) LENGTH: 29 base pairs
314 (B) TYPE: nucleic acid
315 (C) STRANDEDNESS: single
316 (D) TOPOLOGY: linear
317
318 (vi) ORIGINAL SOURCE:
--> 319 (C) ISOLATE: V-alpha-4.4
320
321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
322
323 GAAGCAGCAG AGGGTTTGAA GCCACATAC 29
324

325 (2) INFORMATION FOR SEQ ID NO:8:
326
327 (i) SEQUENCE CHARACTERISTICS:
328 (A) LENGTH: 27 base pairs
329 (B) TYPE: nucleic acid
330 (C) STRANDEDNESS: single
331 (D) TOPOLOGY: linear
332
333 (vi) ORIGINAL SOURCE:
--> 334 (C) ISOLATE: V-alpha-5
335
336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
337
338 GGCAGGTCTT CAGTTGCTTA TGAAGGT 27
339

340 (2) INFORMATION FOR SEQ ID NO:9:

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341
342 (i) SEQUENCE CHARACTERISTICS:
343 (A) LENGTH: 27 base pairs
344 (B) TYPE: nucleic acid
345 (C) STRANDEDNESS: single
346 (D) TOPOLOGY: linear
347
348 (vi) ORIGINAL SOURCE:
--> 349 (C) ISOLATE: V-alpha-6
350
351 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
352
353 GGTTCTCTT CAGGGTCCAG AATATGT 27
354

355 (2) INFORMATION FOR SEQ ID NO:10:
356
357 (i) SEQUENCE CHARACTERISTICS:
358 (A) LENGTH: 27 base pairs
359 (B) TYPE: nucleic acid
360 (C) STRANDEDNESS: single
361 (D) TOPOLOGY: linear
362
363 (vi) ORIGINAL SOURCE:
--> 364 (C) ISOLATE: V-alpha-7
365
366 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
367
368 GCGAAGAACT CACCCTGGAC TGTTTAT 27
369

370 (2) INFORMATION FOR SEQ ID NO:11:
371
372 (i) SEQUENCE CHARACTERISTICS:
373 (A) LENGTH: 30 base pairs
374 (B) TYPE: nucleic acid
375 (C) STRANDEDNESS: single
376 (D) TOPOLOGY: linear
377
378 (vi) ORIGINAL SOURCE:
--> 379 (C) ISOLATE: V-alpha-8
380
381 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
382
383 GAGCTCCACA GACAACAAGA GGACCGAGCA 30
384

385 (2) INFORMATION FOR SEQ ID NO:12:
386
387 (i) SEQUENCE CHARACTERISTICS:
388 (A) LENGTH: 27 base pairs
389 (B) TYPE: nucleic acid
390 (C) STRANDEDNESS: single

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391 (D) TOPOLOGY: linear
392
393 (vi) ORIGINAL SOURCE:
--> 394 (C) ISOLATE: V-alpha-9
395
396 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
397
398 GAGCTGCGAC GTTCCTTAGT GACTGTG 27
399

400 (2) INFORMATION FOR SEQ ID NO:13:
401
402 (i) SEQUENCE CHARACTERISTICS:
403 (A) LENGTH: 30 base pairs
404 (B) TYPE: nucleic acid
405 (C) STRANDEDNESS: single
406 (D) TOPOLOGY: linear
407
408 (vi) ORIGINAL SOURCE:
--> 409 (C) ISOLATE: V-alpha-10
410
411 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
412
413 CCTCGTCAGC CTGTTGTCCA ATCCTTCTGG 30
414

415 (2) INFORMATION FOR SEQ ID NO:14:
416
417 (i) SEQUENCE CHARACTERISTICS:
418 (A) LENGTH: 28 base pairs
419 (B) TYPE: nucleic acid
420 (C) STRANDEDNESS: single
421 (D) TOPOLOGY: linear
422
423 (vi) ORIGINAL SOURCE:
--> 424 (C) ISOLATE: V-alpha-11
425
426 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
427
428 CAGCCTCATC AATCTGTTCT ACTTGGCT 28
429

430 (2) INFORMATION FOR SEQ ID NO:15:
431
432 (i) SEQUENCE CHARACTERISTICS:
433 (A) LENGTH: 28 base pairs
434 (B) TYPE: nucleic acid
435 (C) STRANDEDNESS: single
436 (D) TOPOLOGY: linear
437
438 (vi) ORIGINAL SOURCE:
--> 439 (C) ISOLATE: V-alpha-12
440

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441 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
442
443 CCACCAGGGA CCACAGTTTA TCATTCAA 28
444

445 (2) INFORMATION FOR SEQ ID NO:16:
446
447 (i) SEQUENCE CHARACTERISTICS:
448 (A) LENGTH: 27 base pairs
449 (B) TYPE: nucleic acid
450 (C) STRANDEDNESS: single
451 (D) TOPOLOGY: linear
452
453 (vi) ORIGINAL SOURCE:
--> 454 (C) ISOLATE: V-alpha-14
455
456 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
457
458 ACCTGGAGAG AATCCTAAGC TCATCAT 27
459

460 (2) INFORMATION FOR SEQ ID NO:17:
461
462 (i) SEQUENCE CHARACTERISTICS:
463 (A) LENGTH: 28 base pairs
464 (B) TYPE: nucleic acid
465 (C) STRANDEDNESS: single
466 (D) TOPOLOGY: linear
467
468 (vi) ORIGINAL SOURCE:
--> 469 (C) ISOLATE: V-alpha-15
470
471 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
472
473 AGGTCTTGTG TCCCTGACAG TCCTGGTT 28
474

475 (2) INFORMATION FOR SEQ ID NO:18:
476
477 (i) SEQUENCE CHARACTERISTICS:
478 (A) LENGTH: 30 base pairs
479 (B) TYPE: nucleic acid
480 (C) STRANDEDNESS: single
481 (D) TOPOLOGY: linear
482
483 (vi) ORIGINAL SOURCE:
--> 484 (C) ISOLATE: V-alpha-16
485
486 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
487
488 CAAGCAAACA CTGTAGTGCA GAGCCCTTCC 30
489

490 (2) INFORMATION FOR SEQ ID NO:19:

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491
492 (i) SEQUENCE CHARACTERISTICS:
493 (A) LENGTH: 25 base pairs
494 (B) TYPE: nucleic acid
495 (C) STRANDEDNESS: single
496 (D) TOPOLOGY: linear
497
498 (vi) ORIGINAL SOURCE:
--> 499 (C) ISOLATE: V-alpha-17
500
501 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
502
503 CAAGACATCC ATAAGTGCCC TACAG 25
504

505 (2) INFORMATION FOR SEQ ID NO:20:
506
507 (i) SEQUENCE CHARACTERISTICS:
508 (A) LENGTH: 27 base pairs
509 (B) TYPE: nucleic acid
510 (C) STRANDEDNESS: single
511 (D) TOPOLOGY: linear
512
513 (vi) ORIGINAL SOURCE:
--> 514 (C) ISOLATE: V-alpha-18
515
516 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
517
518 GTGTATGAAA CCCAGGACAG TTCTTAC 27
519

520 (2) INFORMATION FOR SEQ ID NO:21:
521
522 (i) SEQUENCE CHARACTERISTICS:
523 (A) LENGTH: 29 base pairs
524 (B) TYPE: nucleic acid
525 (C) STRANDEDNESS: single
526 (D) TOPOLOGY: linear
527
528 (vi) ORIGINAL SOURCE:
--> 529 (C) ISOLATE: V-alpha-19
530
531 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
532
533 CCGTATTTCT TTCTTATGTT GTTTTGGAT 29
534

535 (2) INFORMATION FOR SEQ ID NO:22:
536
537 (i) SEQUENCE CHARACTERISTICS:
538 (A) LENGTH: 28 base pairs
539 (B) TYPE: nucleic acid
540 (C) STRANDEDNESS: single

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541 (D) TOPOLOGY: linear
542
543 (vi) ORIGINAL SOURCE:
--> 544 (C) ISOLATE: V-alpha-20
545
546 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
547
548 CAAAGCTCTC CATCGCTGAC TGTTC AAG 28
549

550 (2) INFORMATION FOR SEQ ID NO:23:
551
552 (i) SEQUENCE CHARACTERISTICS:
553 (A) LENGTH: 23 base pairs
554 (B) TYPE: nucleic acid
555 (C) STRANDEDNESS: single
556 (D) TOPOLOGY: linear
557
558 (vi) ORIGINAL SOURCE:
--> 559 (C) ISOLATE: V-beta-1
560
561 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
562
563 ATCTAATCCT GGGAAGAGCA AAT 23
564

565 (2) INFORMATION FOR SEQ ID NO:24:
566
567 (i) SEQUENCE CHARACTERISTICS:
568 (A) LENGTH: 23 base pairs
569 (B) TYPE: nucleic acid
570 (C) STRANDEDNESS: single
571 (D) TOPOLOGY: linear
572
573 (vi) ORIGINAL SOURCE:
--> 574 (C) ISOLATE: V-beta-2
575
576 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
577
578 GGCGTCTGGT ACCACGTGGT CAA 23
579

580 (2) INFORMATION FOR SEQ ID NO:25:
581
582 (i) SEQUENCE CHARACTERISTICS:
583 (A) LENGTH: 23 base pairs
584 (B) TYPE: nucleic acid
585 (C) STRANDEDNESS: single
586 (D) TOPOLOGY: linear
587
588 (vi) ORIGINAL SOURCE:
--> 589 (C) ISOLATE: V-beta-3
590

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591 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
592
593 GTGAAAGGGC AAGGACAAAA AGC 23
594

595 (2) INFORMATION FOR SEQ ID NO:26:
596
597 (i) SEQUENCE CHARACTERISTICS:
598 (A) LENGTH: 22 base pairs
599 (B) TYPE: nucleic acid
600 (C) STRANDEDNESS: single
601 (D) TOPOLOGY: linear
602
603 (vi) ORIGINAL SOURCE:
--> 604 (C) ISOLATE: V-beta-4
605
606 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
607
608 GATATGCGAA CAGTATCTAG GC 22
609

610 (2) INFORMATION FOR SEQ ID NO:27:
611
612 (i) SEQUENCE CHARACTERISTICS:
613 (A) LENGTH: 23 base pairs
614 (B) TYPE: nucleic acid
615 (C) STRANDEDNESS: single
616 (D) TOPOLOGY: linear
617
618 (vi) ORIGINAL SOURCE:
--> 619 (C) ISOLATE: V-beta-5.1
620
621 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
622
623 ACATAATCAA AGGAAAGGGA GAA 23
624

625 (2) INFORMATION FOR SEQ ID NO:28:
626
627 (i) SEQUENCE CHARACTERISTICS:
628 (A) LENGTH: 23 base pairs
629 (B) TYPE: nucleic acid
630 (C) STRANDEDNESS: single
631 (D) TOPOLOGY: linear
632
633 (vi) ORIGINAL SOURCE:
--> 634 (C) ISOLATE: V-beta-6
635
636 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
637
638 TCCTGATTGG TCAGGAAGGG CAA 23
639

640 (2) INFORMATION FOR SEQ ID NO:29:

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641
642 (i) SEQUENCE CHARACTERISTICS:
643 (A) LENGTH: 23 base pairs
644 (B) TYPE: nucleic acid
645 (C) STRANDEDNESS: single
646 (D) TOPOLOGY: linear
647
648 (vi) ORIGINAL SOURCE:
--> 649 (C) ISOLATE: V-beta-7
650
651 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
652
653 TACCTGATCA AAAGAATGGG AGA 23
654

655 (2) INFORMATION FOR SEQ ID NO:30:
656
657 (i) SEQUENCE CHARACTERISTICS:
658 (A) LENGTH: 23 base pairs
659 (B) TYPE: nucleic acid
660 (C) STRANDEDNESS: single
661 (D) TOPOLOGY: linear
662
663 (vi) ORIGINAL SOURCE:
--> 664 (C) ISOLATE: V-beta-8.1
665
666 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
667
668 ATAACCATGA CAATATGTAC TGG 23
669

670 (2) INFORMATION FOR SEQ ID NO:31:
671
672 (i) SEQUENCE CHARACTERISTICS:
673 (A) LENGTH: 23 base pairs
674 (B) TYPE: nucleic acid
675 (C) STRANDEDNESS: single
676 (D) TOPOLOGY: linear
677
678 (vi) ORIGINAL SOURCE:
--> 679 (C) ISOLATE: V-beta-8.2
680
681 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
682
683 ATAACCACAA CAACATGTAC TGG 23
684

685 (2) INFORMATION FOR SEQ ID NO:32:
686
687 (i) SEQUENCE CHARACTERISTICS:
688 (A) LENGTH: 23 base pairs
689 (B) TYPE: nucleic acid
690 (C) STRANDEDNESS: single

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691 (D) TOPOLOGY: linear
692
693 (vi) ORIGINAL SOURCE:
--> 694 (C) ISOLATE: V-beta-8.3
695
696 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
697
698 ATAGCCACAA CTACATGTAC TGG 23
699

700 (2) INFORMATION FOR SEQ ID NO:33:
701
702 (i) SEQUENCE CHARACTERISTICS:
703 (A) LENGTH: 23 base pairs
704 (B) TYPE: nucleic acid
705 (C) STRANDEDNESS: single
706 (D) TOPOLOGY: linear
707
708 (vi) ORIGINAL SOURCE:
--> 709 (C) ISOLATE: V-beta-9
710
711 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
712
713 AGCTTGCAAG AGTTGGAAAA CCA 23
714

715 (2) INFORMATION FOR SEQ ID NO:34:
716
717 (i) SEQUENCE CHARACTERISTICS:
718 (A) LENGTH: 23 base pairs
719 (B) TYPE: nucleic acid
720 (C) STRANDEDNESS: single
721 (D) TOPOLOGY: linear
722
723 (vi) ORIGINAL SOURCE:
--> 724 (C) ISOLATE: V-beta-10
725
726 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
727
728 GATTATGTTT AGCTACAATA ATA 23
729

730 (2) INFORMATION FOR SEQ ID NO:35:
731
732 (i) SEQUENCE CHARACTERISTICS:
733 (A) LENGTH: 23 base pairs
734 (B) TYPE: nucleic acid
735 (C) STRANDEDNESS: single
736 (D) TOPOLOGY: linear
737
738 (vi) ORIGINAL SOURCE:
--> 739 (C) ISOLATE: V-beta-11
740

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741 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
742
743 ACAAGGTGAC AGGGAAGGGA CAA 23
744

745 (2) INFORMATION FOR SEQ ID NO:36:
746
747 (i) SEQUENCE CHARACTERISTICS:
748 (A) LENGTH: 23 base pairs
749 (B) TYPE: nucleic acid
750 (C) STRANDEDNESS: single
751 (D) TOPOLOGY: linear
752
753 (vi) ORIGINAL SOURCE:
--> 754 (C) ISOLATE: V-beta-12
755
756 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
757
758 ACCTACAGAA CCAAGGACT CAG 23
759

760 (2) INFORMATION FOR SEQ ID NO:37:
761
762 (i) SEQUENCE CHARACTERISTICS:
763 (A) LENGTH: 23 base pairs
764 (B) TYPE: nucleic acid
765 (C) STRANDEDNESS: single
766 (D) TOPOLOGY: linear
767
768 (vi) ORIGINAL SOURCE:
--> 769 (C) ISOLATE: V-beta-13
770
771 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
772
773 CAGTTGCCCT CGGATCGATT TTC 23
774

775 (2) INFORMATION FOR SEQ ID NO:38:
776
777 (i) SEQUENCE CHARACTERISTICS:
778 (A) LENGTH: 23 base pairs
779 (B) TYPE: nucleic acid
780 (C) STRANDEDNESS: single
781 (D) TOPOLOGY: linear
782
783 (vi) ORIGINAL SOURCE:
--> 784 (C) ISOLATE: V-beta-14
785
786 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
787
788 GCCGAGATCA AGGCTGTGGG CAG 23
789

790 (2) INFORMATION FOR SEQ ID NO:39:

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791
792 (i) SEQUENCE CHARACTERISTICS:
793 (A) LENGTH: 23 base pairs
794 (B) TYPE: nucleic acid
795 (C) STRANDEDNESS: single
796 (D) TOPOLOGY: linear
797
798 (vi) ORIGINAL SOURCE:
--> 799 (C) ISOLATE: V-beta-15
800
801 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
802
803 AGAACCATCT GTAAGAGTGG AAC 23
804

805 (2) INFORMATION FOR SEQ ID NO:40:
806
807 (i) SEQUENCE CHARACTERISTICS:
808 (A) LENGTH: 23 base pairs
809 (B) TYPE: nucleic acid
810 (C) STRANDEDNESS: single
811 (D) TOPOLOGY: linear
812
813 (vi) ORIGINAL SOURCE:
--> 814 (C) ISOLATE: V-beta-16
815
816 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
817
818 CATCAAATAA TAGATATGGG GCA 23
819

820 (2) INFORMATION FOR SEQ ID NO:41:
821
822 (i) SEQUENCE CHARACTERISTICS:
823 (A) LENGTH: 23 base pairs
824 (B) TYPE: nucleic acid
825 (C) STRANDEDNESS: single
826 (D) TOPOLOGY: linear
827
828 (vi) ORIGINAL SOURCE:
--> 829 (C) ISOLATE: V-beta-17
830
831 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
832
833 GTAGTCCTGA AAAAGGGCAC ACT 23
834

835 (2) INFORMATION FOR SEQ ID NO:42:
836
837 (i) SEQUENCE CHARACTERISTICS:
838 (A) LENGTH: 22 base pairs
839 (B) TYPE: nucleic acid
840 (C) STRANDEDNESS: single

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841 (D) TOPOLOGY: linear
842
843 (vi) ORIGINAL SOURCE:
--> 844 (C) ISOLATE: V-beta-18
845
846 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
847
848 CATCTGTCAA AGTGGCACTT CA
849

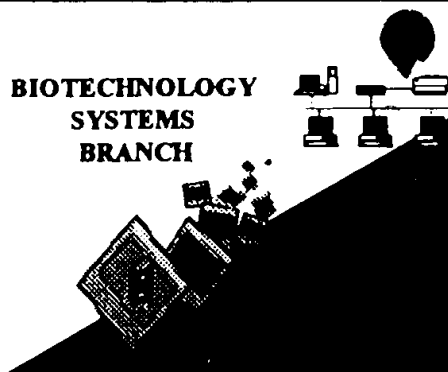
22

1076 (2) INFORMATION FOR SEQ ID NO:51:
1077
1078 (i) SEQUENCE CHARACTERISTICS:
--> 1079 (A) LENGTH: 8 amino acids
1080 (B) TYPE: amino acid
1081 (C) STRANDEDNESS: single
1082 (D) TOPOLOGY: linear
1083
1084
1085 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
1086
1087 His Leu Tyr Gln Gly Gln Trp
1088 1 5
1089

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/812,393DATE: 04/28/98
TIME: 13:04:36

INPUT SET: S25310.raw

Line	Error	Original Text
259	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-1
274	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-2
289	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-3
304	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-4.1.2.3
319	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-4.4
334	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-5
349	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-6
364	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-7
379	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-8
394	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-9
409	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-10
424	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-11
439	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-12
454	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-14
469	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-15
484	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-16
499	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-17
514	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-18
529	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-19
544	Unknown or Misplaced Identifier	(C) ISOLATE: V-alpha-20
559	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-1
574	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-2
589	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-3
604	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-4
619	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-5.1
634	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-6
649	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-7
664	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-8.1
679	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-8.2
694	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-8.3
709	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-9
724	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-10
739	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-11
754	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-12
769	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-13
784	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-14
799	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-15
814	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-16
829	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-17
844	Unknown or Misplaced Identifier	(C) ISOLATE: V-beta-18
1079	Entered (8) and Calc. Seq. Length (7) differ	(A) LENGTH: 8 amino acids



Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF)
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The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CFR 1.821 through 1.825).

Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

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